

Sequence logo showing the conservation of amino acids at positions 100-190, 210-390, and 410-590 across various protein entries. The x-axis represents positions 100 to 590. The y-axis lists protein entries. Each position has four bars representing A, T, C, and G. The height of each bar indicates the frequency of that nucleotide at that position. The sequence logo is color-coded: A (green), T (red), C (blue), and G (yellow).

1400

21221774.b ARRLLCARPGVVFALDPADGSTLWR--HPVEETVRSEPPVVSGGLVQPEVGVLGLPLEALDPATGEPEWQEDMPAYDG-LRTVGDMLLLTRADGMVTGVDSSSGRTRWAHRIPGQAVPYFTSFAGERHAAAYATSQSADGRRTHTVAVDPAGGDVWRDTELAGALTPTVGTADGSVFLVVBGATYGDVTAVVRYTPAT
29831260.b PHRLYCTRPGVLAADVAPDGKVLWSRGDAKRHSRGDTVR--PPVLSGGLLHVSEGKRLAALDPATGKTRWSHDLAAYGGRFAQVGGVLLLTGADARVTALEDAATGEEKWRRIPIQPQPAFVSYG--DGLAYAVAAMASG--TKVAADVDPESGAIRWORRFDGVLISLVGAIDGAVWFASTADS-DTDAVVRDVIR
1mrn_PKN

29830627.b ...
2122057.b PAPRGTSAASRGSSAERGS--VPERGGAPSRGGTPSRGGTPS--GGGGASGPSSSSSAGAASQKVPAYIENDRISRDNTWLSDNFDDAANGIKCAQIGAVASAPEELQYSARDADDPQPLAYKEKAKISFRFKYAEKLNNKPEPYVVSVGVKPPHDIDSSETGKPYEVMAANKTIGYSSKP
21222037.b TGGGP--GGTSSRGRTGARSGSPPTPDRTT--GRNRSRNDRGCRFAPIRGGSRTAPR-TTCGTRRFPAN_RLRLQRFLFVEVVVTLV
29833341.b BPPR--TSRSRGTGTTT--RNSTRS-GSRPASRGAQGRSSPR-TTGTG-RPAN_RLRLQRFLFVEVVVTLV
21222892.b GPPDDDFGAGTGTTRPP--GRLALSVAATSTQGAQGRGRRIISCTVALAVAGALAATVGSVFLDLPLG--SGNDANN--AGGNEASHDPPAATP-GGLPARLYGTWEQAAALDGKLPGLTFRITIKQAKAQGELGRLRQTDALGCVCDVITLKKVT
29831365.b DAEVGVFLAVLPESGPP--GRFVSVVAATSAFPTGGRGRVSVCTVALAVAGALATVGSVFLDLPLG--SGDSSGASDPSAASDPEAALDSDPQDGDAD--GAVPKVSYLGTBEGDALALGGTLPAGTRVITGAEVKELGTRSTQDQGKCDVLLRKAT
21222037.b PAPOGYDPAWAHSQCG--HQHYDGGGGLGPPTPPGPPP-EYGPHEPVNRGRSTALLIVVVALVVALCAGGSVYALMKGDDGRAGGDPPTTRSTGQPDFTGTCAGSSG-ATGCRSPTGPAADE-GTVPVTCYLGDWSTSIDSNAHGTHPR--TLLIVEVGEVDLTVLVA
29831097.b HPQQHQPQPSAYGYQNAGWGGAPAYGGPGLGSPPTPYGPVVGAPGQPEPPRSRGSSTAALIVVVALVVALCAGGSVYALMKGDDGRAGGDPPTTRSTGQPDFTGTCAGSSG-ATGCRSPTGPAADE-GTVPVTCYLGDWSTSIDSNAHGTHPR--TLLIVEVGEVDLTVLVA
32141238.b AASAPGFKASRRTATPD--QDRSASFSRSPGEGQGDRRGADAGGGAGGSQGDADAGGAGSGSGSGSGAGGGAGSGSGSGADSGSGSGSGSGSGSG--SGDGGASGSGVFTLNKNAKNGRCCLTTAHADAFYDCTGDAATWTFRSPDGTWINGLLGR
21222874.b AASATGP--SASASPS-PDGKKKDDQDKDKDRKQGQDGGAPGGG-GSCDAAAAAAGASGGGSDSGASGSGSSGGGGSGAGGTSASGSGSSGACDGTDGAGS--EGGGSSASDEFMNKNGSGXCKMVVG-TFVDDGACSGDVAVEFRFQSTSGCAFIRLNVCAOC
32141236.b EASAPGVRPRAFRMSNDVWGTPTRAVEDLWVITSFEVHALDVATGRRFKTRDVAWSMAVADGRHAASGPTLTFALDAREGADLWVQTDIAWVYSLOADRGTVLTAATRGVYVAAQEDFESPEAALHDTGAYVWQDARLRAFDLARQDG
29830359.b AEASAGWVPRFRMSNDVWGTPTRAVEDLWVITSFEVHALDVATGRRFKTRDVAWSMAVADGRHAASGPTLTFALDAREGADLWVQTDIAWVYSLOADRGTVLTAATRGVYVAAQEDFESPEAALHDTGAYVWQDARLRAFDLARQDG
21222873.b TATGDLGGR--RSRRAFLFSCAGALAAALGVGTGFWLNRPAIDPDAECSAP--APSFSAPSPPPGFGVGLWPLDEASQGVARDTAGHDGTGTVG--VANQGAGEAATDGTGSQIVT--AGFVLQTGACRSPTAAWVRLSAVFGVFAVASQ-DSADA
21222767.b GGPFPVPR--PDGFERRRRNRNARVLTAAAVVACGLVIAAATGALLDAAGR--LDRDRAVASASGTPRVAEGAASAGEAESTG--PQAASADTSDTGSDGPTATTAPAAHAYAPMLDNDSLILHNKESKDQRKGDIREFGCENAC
32465243.b DFTDAGTQVLGATTFMPDQTTPLAERTTLPQPSFPPSGTAQSSWDPAQNSQPTAVDPAIRPALQRIIDQTAQAAPTETMVQNPPMPNPVFDVKRGEYLQRTLPILLAAAPLAALAAANAPLVAIAATALLWLLTLYNTEPQLEREGKRGGERKNSD
21242656.b ...
21224924.b PTAGFLDYYATRLGKATADRLLRDLPTAAVLAELGALTVPAGVADWDERRMVLEAAAASVNAAATPRLIEYPRDLSLVRAIRLTLQACLVRWIVLGVIEGRPQGLTGEDVHRYRARFPELVVWDPGRGGTAHEPLTAGFLKALRDAGFELSL
2phk_PHK

113r_PKA EFTEF

2erk_Erk2

1jwh_CKII

lias_TGFbR

1600

21221774.b GATRRVILDPIPVEQA-SASACVREDTVILMAGGSLVADVMAAEKCAWRLETVGERSGAPVSDGRHVVTAPDGRLLGVDAKRCKLIGQTRPRLGADSDTVPASLAPLLAGHHVYAGAPDGTWFGVAGRDPGGW
29831260.b RTVRRVCLRFPLQG-AQAVVRKDVTVVLANGGALVADTRTSKELWRLTEVSFASAPVAAGDRVYFAGADGRLLAVDASKCQVLLGQTKARLGGAHGSILSGLSPVVAADGVYVSAAPDGSFLAVDARPPGG
1mrn_PKN

29830627.b ...
2122050.b ALG--IAAAQGQQGPARCLGDERGGVRAATQRQDVPFGGLPPEPRTGR
29833341.b ALG--IAAAQGQQGPARCLDD--GGVRKD--VREQES--YEWPR-GI
21222892.b EK--QLVAGSAGAEGNHDCNPA-PTTVTFVGDDLDYASKSEESGRPTARLSKVG
29831365.b AQ--QLVATSVAKDTINQACGNPTSRTG-RHEVRLTFVGDDLDYSETDNRGKMSKVK
21222037.b AEPGSG--GPLRQPSAVRIG-PASSCAGGGPSTVILR-DGSLERTSDTIGESLLYTRAGGY
29831097.b EKPGSD--GPLEIGPSTVTVGEFPAASSCTPGDASEIIILPDGS-LRRLVKGITSEALTYIKSD
32141238.b IYTAIIGHPVFSPFC--GRITQEVWVGSGGTLKNAATGGCVTVS-AMSGTGVNACEQSAQRWIRS
21222874.b IHGSRSANALVWKDTC--G-SFGGEWCEGASGLRNLIAGGCLDINRRAASMIGLTTTCGSDQQRWIRT
32141236.b ALEVASGHRWHPFEAAPAVFLAPPFTVPGPAVTGGVYIADYLGTVXALDAJDGRDRWRIATEARSSSTDPLVVAAGHVHVSGSKGLYTLDAVIGT-KWRFQAGGDIVGAPAAVEBCRHFHGSSDHLLYTLKADDGRLRWLKATGGEITGA
29830359.b AVDIAGGHRWHPFEAAPAVFLSPPTFVPGPAVAGGGCITYLADYLGTVYALDAJDGRDRWRIATESRASLDPLVVAAGHVHVSGSKGLYTLDAVIGT-KWRFQAGGDIVGAPAAVEBCRHFHGSSDHLLYTLKADDGRLRWLKATGGEITGA
21222873.b GRTAPAAHHVTHLHG--VCDGFPARKLHLYVNGVCEAVVREDIGPAPATGAFMICRASFDQCPDRFFG
21222767.b ELKSDTSVMENVVLG--PGATYETCRRLTSDEA-RELLLAKAAGSEICVKHRNGDIALLVIQVK5-TAMREDGFLTFDITVWPAAG
21242656.b TAALALPVHTISWYFTADWG--IPVPLINDVFSASGLALGGFMAIGWLVTVFVQPSMMIRLGGGVLRGLKHSPAGAPSTEVGGAPPAPVAPAKGGGRGTVLFTIMAIITVALCAMPILGMPINWMPA
21224924.b GAVRAEERLLASASAHDRGCVRVLTVRQLVDRAYRELGAERLGGQQAVSVTELFLAEALHGGVTPGKPTWETLLKADAAEPGSKGAVRFAEYARTAWGSVEPRIAELLGDGGGAGVFLTEAGVFA
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113r_PKA

2erk_Erk2

1jwh_CKII

lias_TGFbR

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21224924.b DAK
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2erk_Erk2

1jwh_CKII

lias_TGFbR